

Figure 1 – Human STR_50E1 – SEQ ID NO:1Nucleotide sequence of long splice variant

[initiation ATG and stop codons are underlined]

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GGGCTCCCTG CACAAATGCG TTGGGTGATG GGGGCTGAAT CCAGCCCACA CTGCACTTGC CAAGCCAGCT 70
GGGGCCCTGG CACAAGACAG TCCCAGCCTG TTTTCACTGA CTTTGCTAAT TCTCACGGAG GCACCATGTG 140
GTGTGGGAAG GCCCGGTCTT CGTAACCTCT CTGCTCCCAG GTCCCTGACC AGTCCTTAAC ACACAGTGGT 210
CTTTGCTCAC CTGCGGCCCA GCTCTGGGCT CTCCCCAAG CATCCTTTGC CTTGCCTCCC TCCCATCTTC 280
CTCTGGGCCT TCTCTCTGCT CCTGCCAGG AAAGTGTGCT CTCAGGAGCG CAGGAGCCAG CTCTCAGCCC 350
CCATCTCCTG GGCACCTACC GTACTCAGGA AATATGTTCT GAATTCAGGA TTATCCTCAT TCTACTGAGA 420
AGACCTGGAG GACAGAAATC AGCAAGACCT AAAGGGGAGA GGAAGGAGGG CCAGGCTGGG GTGGAGGTGC 490
CCCACCCGGG AGCCCGGGCG CAGCCTCACC GCAGGCTGAT TCACAGAAGG CTCAGAGGGT TGCGAGGGCC 560
CAATCGGCAC TGTCATCTG CCCAGGCTCT GAGTCACCAG CTGGTGAGGG GCAGCTGCAG CCCAGCAGGA 630
AACAAAGTCT AGCAATGGGAAG AGGTGGGAGG GAGGTGGTGG GGCCTGAAAC CCCGCTGGC TGGCCTTAGA 700
GGAAGTGGGA GTGACTGTCC GGCACCTGCT CAGCAGCAA CAGCTCTCAA GGACGTGCTA GGAGTCAGGA 770
ACTGGGCCAG CTCCGGTCCC TTCCTTTTGG GGCTCTCACT CTGGAGGATG GGGTGGATGG GAGGTCAGAG 840
GAGCACCAGC CTATGGCCCT GGACACCTGG GGTATTCAGC GAGTTCCTGG AGGACGGTGG GATGGGGCTG 910
TGTTTCCAGC AAGAAAAAAC CGGAAGATC CTGACGGAGT TCCTCCAGTT CTATGAAGAC CAGTATGGCG 980
TGCTCTCTT CAACAGCATG CGCCATGAGA TTGAGGGCAC GGGGCTGCCG CAGGCCCAGC TGCTCTGGCG 1050
CAAGGTGCCA CTGGACGAGC GCATCGTCTT CTCGGGGAAC CTCTTCCAGC ACCAGGAGGA CAGCAAGAAG 1120
TGAGAAACC GCTTCAGCCT CGTGCCCCAC AACTACGGG TGGTGCTCTA CGAAAACAA GCGGCCTATG 1190
AGCGGCAGGT CCCACCAGA GCGTCATCA ACAGTGCAGG CTACAAAATC CTCACGTCCG TGAACCAATA 1260
CCTGGAGCTC ATTGGCAACT CCTTACCAGG GACCACGGCA AAGTCGGGCA GTGCCCCCAT CCTCAAGTGC 1330
CCCACACAGT TCCCCTCAT CCTCTGGCAT CCTTATGCGC GTCACCTACTA CTTCTGCATG ATGACAGAAG 1400
CCGAGCAGGA CAAGTGGCAG GCTGTGCTGC AGGACTGCAT CCGGCACTGC AACAAATGGA TCCCTGAGGA 1470
CTCCAAGSTA GAGGGCCCTG CGTTCACAGA TGCCATCCGC ATGTACCGAC AGTCCAAGGA GCTGTACGGC 1540
ACCTGGGAGA TGCTGTGTGG GAACGAGGTG CAGATCCTGA GCAACCTGGT GATGGAGGAG CTGGGCCCTG 1610
AGCTGAAGGC AGAGCTCGGC CCGCGGCTGA AGGGGAAACC GCAGGAGCGG CAGCGGCAGT GGATCCAGAT 1680
CTCGGACGCC GTGTACCACA TGGTGACGA GCAGGCCAAG GCGCGCTTCG AGGAGGTGCT GTCCAAGGTG 1750
CAGCAGGTGC AGCCGGCCAT GCAGGCCGTC ATCCGAAGTG ACATGGACCA AATTATCACC TCCAAGGAGC 1820
ACCTTGCCAG CAAGATCCGA GCCTTCATCC TCCCCAAGGC AGAGGTGTGC GTGCGGAACC ATGTCCAGCC 1890
CTACATCCCA TCCATCCTGG AGGCCCTGAT GGTCCCCACC AGCCAGGGCT TCACTGAGGT GCGAGATGTC 1960
TTCTTCAAGG AGGTCACGGA CATGAACCTG AACGTATCA ACGAGGGCGG CATTGACAAG CTGGGCGAGT 2030

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ACATGGAGAA GCTGTCCCGG CTGGCGTACC ACCCCCTGAA GATGCAGAGC TGCTATGAGA AGATGGAGTC 2100
 GCTGCGACTG GACGGGCTGC AGCAGCGATT TGATGTGTCC AGCACGTCCG TGTCAAGCA GCGAGCCCAG 2170
 ATCCACATGC GGGAGCAAAT GGACAATGCC GTGTATACGT TCGAGACCCT CCTGCACCAG GAGCTGGGGA 2240
 AGGGGCCCCAC CAAGGAGGAG CTGTGCAAGT CCATCCAGCG GGTCTTGGAG CGGGTGCTGA AAAAATACGA 2310
 CTACGACAGC AGCTCTGTGC GGAAGAGGTT CTTCCGGGAG GCGCTGCTGC AGATCAGCAT CCCGTTCTCTG 2380
 CTCAAGAAGC TGGCCCCCTAC CTGCAAGTCG GAGCTGCCCC GGTTCAGGA GCTGATCTTC GAGGACTTTG 2450
 CCAGGTTTCAT CCTGGTGGAA AACACGTACG AGGAGGTGGT GCTGCAGACC GTCATGAAGG ACATCCTGCA 2520
 GGCTGTGAAG GAGGCCGCGG TGCAAGGAA GCACAACCTC TACCGGGACA GCATGGTCAT GCACAACAGC 2590
 GACCCCAACC TGCACCTGCT GGCCGAGGGC GCCCCATCG ACTGGGGCGA GGAGTACAGC AACAGCGGCG 2660
 GGGGCGGCAG CCCCAGCCCC AGCACCCCGG AGTCAGCCAC CCTCTCGGAA AAGCGACGGC GCGCCAAGCA 2730
 GGTGGTCTCT GTGGTCCAGG ATGAGGAGGT GGGGCTGCCC TTTGAGGCTA GCCCTGAGTC ACCACCACCT 2800
 GCGTCCCCCG ACGGTGTCAC TGAGATCCGA GGCCTGCTGG CCCAAGGTCT GCGGCCTGAG AGCCCCCAGC 2870
 CAGCCGGCCC CCTGCTCAAC GGGGCCCCCG CTGGGGAGAG TCCCCAGCCT AAGGCCGCCC CCGAGGCCCTC 2940
 CTCGCCGCTT GCCTCACCCC TCCAGCATCT CTGCGCTGGA AAGGCTGTGG ACCTTGGGCC CCCCAGGCC 3010
 AGCGACCAGG AGACTGGAGA GCAGGTGTCC AGCCCCAGCA GCCACCCCGC CCTCCACACC ACCACCGAGG 3080
 ACAGTGCAGG GGTGCAGACT GAGTTCTAGG CCAGTGGGTC CCTGACTGCT GCACATGGCA GAGGCCGTTT 3150
 CCTTCCGGAC CCAGGCAGGC TCAGCTCTGG GGAGGACACC CTGGTCTGTG CCTTGTGGGT GGAGGCGGGG 3220
 CAGGGCTGTG TGCACCGCC AGGGAGCGGG CCCACCTGAG TCACTTTATT GGGTTCAGTC AACACTTTCT 3290
 TGCTCCCTGT TTTCTCTTCT GTGGGATGAT CTCAGATGCA GGGGCTGGTT TTGGGGTTT CCTGCTTGTG 3360
 CCAAGGGCTG GACACTGCTG GGGGGCTGGA AAGCCCCTCC CTTCTGTCC TTCTGTGGCC TCCATCCCCT 3430
 CATGGGTGCT GCCATCCTTC CTGGAGAGAG GGAGGTGAAA GCTGGTGTGA GCCAGTGGG TTCCCGCCCA 3500
 CTCACCCAGG AGCTGGCTGG GCCAGGACCG GGAGAGGGAG CACTGCTGCC CTCCTGGCCC TGCTCCTTCC 3570
 GCACTTAGGG GTGGACCGAG CCTCGCTTTC CCCACTGTTC TGGAGGGAAG GGAAGGAGG GGTCTTCAG 3640
 GCTGGAGCCA GGCTGGGGGT GCTGGGTGGA GAGATGAGAT TTAGGGGGTG CCTCATGGG TGGGCAGGCC 3710
 TGGGGTGAAA TGAGAAAGGC CCAGAACGTG CAGGTCTGCG GAGGGGAAGT GTCCTGAGTG AAGGAGGGGA 3780
 CCCCATCCTG GGGATGCTGG GAGTGAGTGA GTGAGATGGC TGAGTGAGGG TTATGGGGAG CCTGAGGTTT 3850
 TATGGGCCTG TGATCCCCT TCTCCCGGCC CCAGCCTGCC TCCCTCCTGC CCGCCTGGCC CACAGGTCTC 3920
 CCTCTGGTCC CTGTCCCTCT GGTGGTTGGG GATGGAGCGG CAGCAAGGGG TGTAATGGGG CTGGGTTCTG 3990
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 CTCCTCTGA AAATCCAGTC CCTTCTTTGG ATGTCCTTGT GAGTCACTCT GGGCTGGCT GTCGTCCCTC 4200
 CTCAGCTTCT TGTCCTGGG ACAAGGTCA AGCCAGGATG GGCCAGGCN TGGGATCCCC CACCCAGGA 4270
 CCCCACAGGC CCCCTCCCCT GNTGNTTTGC GGGGGCAGG GCAGAAATGG ACTCCTTTTG GTCCCCGAG 4340
 GTGGGGTCCC CTCCAGCCC TGCATCCTCC GTGCCCTAGA CCTGCTCCCC AGAGGAGGGG CCTTGACCCA 4410

CAGGAAGTGT GGTGGCGCCT GGCAATCAGG GACCCCCAGC TGCCGCAGCC CTGGTTTTTG GCGCATCTTT 4480
TCCCTCTTGT CCCGAAGATT TGCGCCTTTA GTGCCTTTTG AGGGGTTCCTC ATCATCCCTC CCTGATATTG 4550
TATTGAAAAT ATTATGCACA CTGTTTCATGC TTTACTAAT CAATAACGC TTTATTTAAA AAAAAAAAAA 4620
AAA 4623

Figure 2 – Human STR_50E1 – SEQ ID NO:2Predicted polypeptide of long splice variant

(Alternatively-spliced exon is marked)

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MEEVGGRWWG LKPRLAGLRG TGSDCPALAQ QQTALKDVLG VRNWASSGPF LLGLSLWRMG WMGQQRSTSL 70
WPWTPGVFSE FLEDGGMGLW FQQEKTGKIL TEFLQFYEDQ YGVALFNSMR HEIEGTGLPQ AQLLWRKVPL 140
DERIVFSGNL FQHQEDSKKW RNRFSLVPHN YGLVLYENKA AYERQVPPRA VINSAGYKIL TSVDQYLELI 210
GNSLPGTTAK SGSAPILKCP TQFPLILWHP YARHYFMM TEAEQDKWQA VLQDCIRHCN NGIPEDSKVE 280
GPAFTDAIRM YRQSKELYGT WEMLCGNEVQ ILSNLVMEEL GPGLKAEELG RLKGGKQERQ RQWQISDAV 350
YHMVYEQAKA RFEEVLISKVQ QVQPMQAVI RTDMDQIITS KEHLASKIRA FILPKAEVCV RNHVQPYIPS 420
ILEALMVPTS QGFTEVRDVF FKEVTDMLN VINEGGIDKL GEYMEKLSRL AYHPLKMQSC YEKMESLRD 490
GLQQRFDVSS TSVFKQRAQI HMREQMDNAV YTFETLLHQE LGKGPTKEEL CKSIQVLER VLKDYDYSS 560
SVRKRFFREA LLQISIPFL KKLAPTCKSE LPRFQELIFE DFARFILVEN TYEEVVLQTV MKDILQAVKE 630
AAVQRKHNLV RDSMVMHNSD PNLHLAEGA PIDWGEEYSN SGGGGSPSPS TPESATLSEK RRRAKQVSV 700
VQDEEVGLPF EASPESPPA SPDGVTEIRG LLAQGLRPES PPPAGPLNG APAGESPQPK AAPEASSPPA 770
SPLQHLLPGK AVDLGPPKPS DQETGEQVSS PSSHPALHTT TEDSAGVQTE F 821.

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Figure 3 – Human STR_50E1 – SEQ ID NO:3Nucleotide sequence of short splice variant

(Initiation ATG and stop codons are underlined)

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GGGCTCCCTG CACAATGCG TTGGGTGATG GGGGCTGAAT CCAGCCCACA CTGCACTTGC CAAGCCAGCT 70
GGGGCCCTGG CACAAGACAG TCCCAGCCTG TTTTCACTGA CTTTGCTAAT TCTCACGGAG GCACCATGTG 140
GTGTGGGAAG GCCCGGTCTT CGTAACCTCT CTGCTCCCAG GTCCCTGACC AGTCCTTAAC ACACAGTGGT 210
CTTTGCTCAC CTGCGGCCCA GCTCTGGGCT CTCCCCACAG CATCCTTTGC CTGCGCTCCC TCCCATCTTC 280
CTCTGGGCCT TCTCTCTGCT CCTGCCCAGG AAAGTGTGCT CTCAGGAGCG CAGGAGCCAG CTCTCAGCCC 350
CCATCTCCTG GGCACTCACC GTACTCAGGA AATATGTTCT GAATTCAGGA TTATCCTCAT TCTACTGAGA 420
AGACCTGGAG GACAGAAATC AGCAAGACCT AAAGGGGAGA GGAAGGAGGG CCAGGCTGGG GTGGAGGTGC 490
CCCACCCGGG AGCCCGGGCG CAGCCTCACC GCAGGCTGAT TCACAGAAGG CTCAGAGGGT TGGGAGGGCC 560
CAATCGGCAC TGTATCCTG CCCAGGCTCT GAGTCACCAG CTGGTGAGGG GCAGCTGCAG CCCAGCAGGA 630
AACAAAGTCT AGCATGGAAG AGGTGGGAGG GAGGTGGTGG GGCCTGAAAC CCCGCCTGGC TGGCCTTAGA 700
GGAAGTGGGA GTGACTGTCC GGCACCTGGT CAGCAGCAAA CAGCTCTCAA GGACGTGCTA GGAGTCAGGA 770
ACTGGGCCAG CTCCGGTCCC TTCTTTTGG GGCTCTCACT CTGGAGGATG GGGTGGATGG GAGAAAAAAC 840
CGGGAAGATC CTGACGGAGT TCCTCCAGTT CTATGAAGAC CAGTATGGCG TGGCTCTCTT CAACAGCATG 910
CGCCATGAGA TTGAGGGCAC GGGGCTGCCG CAGGCCCAGC TGCTCTGGCG CAAGGTGCCA CTGGACGAGC 980
GCATCGTCTT CTCGGGGAAC CTCTTCCAGC ACCAGGAGGA CAGCAAGAAG TGGAGAAACC GCTTCAGCCT 1050
CGTGCCCCAC AACTACGGGC TGGTGCTCTA CGAAAACAAA GCGGCCTATG AGCGGCAGGT CCCACCACGA 1120
GCCGTCATCA ACAGTCAGG CTACAAAATC CTCACGTCCG TGGACCAATA CCTGGAGCTC ATTGGCAACT 1190
CCTTACCAGG GACCACGGCA AAGTCGGGCA GTGCCCCCAT CCTCAAGTGC CCCACACAGT TCCCGCTCAT 1260
CCTCTGGCAT CCTTATGCGC GTCACTACTA CTTCTGCATG ATGACAGAAG CCGAGCAGGA CAAGTGGCAG 1330
GCTGTGCTGC AGGACTGCAT CCGGCACTGC AACAATGGAA TCCCTGAGGA CTCCAAGGTA GAGGGCCCTG 1400
CGTTCACAGA TGCCATCCGC ATGTACCGAC AGTCCAAGGA GCTGTACGGC ACCTGGGAGA TGCTGTGTGG 1470
GAACGAGGTG CAGATCTGA GCAACCTGGT GATGGAGGAG CTGGGCCCTG AGCTGAAGGC AGAGCTCGGC 1540
CCGCGGCTGA AGGGGAAACC GCAGGAGCGG CAGCGGCAGT GGATCCAGAT CTCGGACGCC GTGTACCACA 1610
TGGTGACGA GCAGGCCAAG GCGCGCTTCG AGGAGGTGCT GTCCAAGGTG CAGCAGGTGC AGCCGGCCAT 1680
GCAGGCCGTC ATCCGAACTG ACATGGACCA AATTATCACC TCCAAGGAGC ACCTTGCCAG CAAGATCCGA 1750
GCCTTCATCC TCCCCAAGGC AGAGGTGTGC GTGCGGAACC ATGTCCAGCC CTACATCCCA TCCATCCTGG 1820
AGGCCCTGAT GGTCCCCACC AGCCAGGGCT TCACTGAGGT GCGAGATGTC TTCTTCAAGG AGGTCACGGA 1890
CATGAACCTG AACGTCATCA ACGAGGGCGG CATTGACAAG CTGGGCGAGT ACATGGAGAA GCTGTCCCGG 1960
CTGGCGTACC ACCCCCTGAA GATGCAGAGC TGCTATGAGA AGATGGAGTC GCTGCGACTG GACGGGCTGC 2030

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AGCAGCGATT TGATGTGTCC AGCACGTCCG TGTTC AAGCA GCGAGCCCAG ATCCACATGC GGGAGCAAAT 2100
 GGACAATGCC GTGTATACGT TCGAGACCCT CCTGCACCAG GAGCTGGGGA AGGGGCCAC CAAGGAGGAG 2170
 CTGTGCAAGT CCATCCAGCG GGTCTGGAG CGGGTGCTGA AAAAATACGA CTACGACAGC AGCTCTGTGC 2240
 GGAAGAGGTT CTTCCGGGAG GCGCTGCTGC AGATCAGCAT CCCGTTCTTG CTCAAGAAGC TGGCCCTAC 2310
 CTGCAAGTCG GAGCTGCCCC GGTTCAGGA GCTGATCTTC GAGGACTTTG CCAGGTTTCAT CCTGGTGGAA 2380
 AACACGTACG AGGAGGTGGT GCTGCAGACC GTCATGAAGG ACATCCTGCA GGCTGTGAAG GAGGCCGCGG 2450
 TGCAGAGGAA GCACAACCTC TACCGGGACA GCATGGTCAT GCACAACAGC GACCCCAACC TGCACCTGCT 2520
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 AGCACCCCGG AGTCAGCCAC CCTCTCGGAA AAGCGACGGC GCGCCAAGCA GGTGGTCTCT GTGGTCCAGG 2660
 ATGAGGAGGT GGGGCTGCCC TTTGAGGCTA GCCCTGAGTC ACCACCACCT GCGTCCCCGG ACGGTGTCAC 2730
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 GGGGCCCCCG CTGGGGAGAG TCCCCAGCCT AAGGCCGCC CCGAGGCCTC CTCGCCGCTT GCCTCACCCC 2870
 TCCAGCATCT CCTGCCTGGA AAGGCTGTGG ACCTTGGGCC CCCAAGCCC AGCGACCAGG AGACTGGAGA 2940
 GCAGGTGTCC AGCCCCAGCA GCCACCCGCG CCTCCACACC ACCACCGAGG ACAGTGCAGG GGTGCAGACT 3010
 GAGTTCTAGG CCAGTGGGTC CCTGACTGCT GCACATGGCA CAGGCCGTTT CCTTCCGGAC CCAGGCAGGC 3080
 TCAGCTCTGG GGAGGGCACC CTGGTCTGTG CCTTGTGGGT GGAGGCGGGG CAGGGCTGTG TGGCACCGCC 3150
 AGGGAGCGGG CCCACCTGAG TCACTTTATT GGGTTCAGTC AACACTTTCT TGCTCCCTGT TTTCTCTTCT 3220
 GTGGGATGAT CTCAGATGCA GGGGCTGGTT TTGGGGTTTT CTGCTTGTG CCAAGGGCTG GACACTGCTG 3290
 GGGGGCTGGA AAGCCCTCC CTTCTGTGCC TTCTGTGGCC TCCATCCCT CATGGGTGCT GCCATCCTTC 3360
 CTGGAGAGAG GGAGGTGAAA GCTGGTGTGA GCCAGTGGG TTCCCGCCCA CTCACCCAGG AGCTGGCTGG 3430
 GCCAGGACCG GGAGAGGGAG CACTGTGCC CTCCTGGCCC TGCTCCTTCC GCAGTTAGGG GTGGACCGAG 3500
 CCTCGCTTTC CCCACTGTTC TGGAGGAAG GGAAGGAGG GGGTCTTCAG GCTGGAGCCA GGCTGGGGGT 3570
 GCTGGGTGGA GAGATGAGAT TTAGGGGTG CCTCATGGG TGGGCAGGCC TGGGGTGAAA TGAGAAAGGC 3640
 CCAGAACGTG CAGGTCTGCG GAGGGGAAGT GTCCTGAGTG AAGGAGGGA CCCATCCTG GGGATGCTGG 3710
 GAGTGAGTGA GTGAGATGGC TGAGTGAGG TTATGGGAG CCTGAGTTT TATGGGCTG TGTATCCCT 3780
 TCTCCCGGCC CCAGCCTGCC TCCCTCCTGC CCGCCTGGCC CACAGGTCTC CCTCTGGTCC CTGTCCCTCT 3850
 GGTGGTTGGG GATGGAGCGG CAGCAAGGG TGTAATGGG CTGGGTCTG TCTTCTACAG GCCACCCGA 3920
 GGTCTCAGT GGTTCCTGG GGAGCCGAC GGGGCTCCTG AGGGGTACAG GTTGGGTGG CCCTCCCTGA 3990
 GGGTCTGGG TCAGGCTTG GCCTCTGCTG CCTCTCAGTC ACCAAGTCAC CTCCTCTGA AAATCCAGTC 4060
 CCTTCTTTGG ATGTCCTTGT GAGTCACTCT GGGCCTGGCT GTCGTCCCTC CTCAGCTTCT TGTTCTGGG 4130
 ACAAGGTCA AGCCAGGATG GGCCAGGCN TGGGATCCCC CACCCAGGA CCCACAGGC CCCCTCCCT 4200
 GNTGNTTTC GGGGGCAGG GCAGAAATGG ACTCCTTTT GGTCCCCGAG GTGGGGTCCC CTCCCAGCCC 4270
 TGCATCCTCC GTGCCCTAGA CCTGCTCCCC AGAGGAGGGG CCTTGACCCA CAGGAAGTGT GGTGGCGCCT 4340
 GGCAATCAGG GACCCCAAGC TGCCGAGCC CTGGTTTTT GCGCATCTTT TCCCTCTGT CCCGAAGATT 4410

TGCGCCTTTA GTGCCTTTTG AGGGGTCCC ATCATCCCTC CCTGATATTG TATGAAAAT ATTATGCACA 4480
CTGTTTCATGC TTTTACTAAT CAATAACGC TTTATTTAAA AAAAAAAAAA AAA 4533

Figur 4 – Human STR_50E1 – SEQ ID NO:4Predicted polypeptide of short splice variant

MEEVGGRWWG LKPRLAGLRG TGSDCPALAQ QQTALKDVLG VRNWASSGPF LLGLSLWRMG WMGEKTGKIL 70
TEFLQFYEDQ YGVALFNSMR HEIEGTGLPQ AQLLWRKVPL DERIVFSGNL FQHQEDSKKW RNRESLVPHN 140
YGLVLYENKA AYERQVPPRA VINSAGYKIL TSVDAQYLELI GNSLPGTAK SGSAPILKCP TQFPLILWHP 210
YARHYFCMM TEAEQDKWQA VLQDCIRHCN NGIPEDSKVE GPAFTDAIRM YRQSKELYGT WEMLCGNEVQ 280
ILSNLVMEEL GPELKAEELG RLKGPQERQ ROWIQISDAV YHMVYEQAKA RFEEVLSKVQ QVQPAMQAVI 350
RTDMDQIITS KEHLASKIRA FILPKAEVCV RNHVQPYIPS ILEALMVPTS QGFTEVRDVF FKEVTDMLN 420
VINEGGIDKL GEYMEKLSRL AYHPLKMQSC YEKMESLRD GLQQRFDVSS TSVFKQRAQI HMREQMDNAV 490
YTFETLLHQE LGKGPTKEEL CKSIQVLER VLKKYDYDSS SVRKRFFREA LLQISIPFL KKLAPTCKSE 560
LPRFQELIFE DFARFILVEN TYEEVVLQTV MKDILQAVKE AAVORKHNLY RDSMVMHNSD PNLHLLAEGA 630
PIDWGEEYSN SGGGGSPPSPS TPESATLSEK RRRAKQVVS VQDEEVGLPF EASPESEPPA SPDGVTEIRG 700
LLAQGLRPES PPPAGPLLNG APAGESPQPK APEASSPPA SPLQHLPGK AVDLGPPKPS DQETGEQVSS 770
PSSHPALHTT TEDSAGVQTE F 791